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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/015,389A

DATE: 07/10/2002 P.6
TIME: 15:15:30

Input Set : A:\GENENLAW-#104456-v1-
 _C48__corrected_sequence_listing.P1C48.txt
 Output Set: N:\CRF3\07102002\J015389A.raw

3 <110> APPLICANT: Baker, Kevin P.
 4 Botstein, David
 5 Desnoyers, Luc
 6 Eaton, Dan I.
 7 Ferrara, Napoleone
 8 Fong, Sherman
 9 Gao, Wei-Qiang
 10 Goddard, Audrey
 11 Godowski, Paul J.
 12 Grimaldi, Christopher J.
 13 Gurney, Austin L.
 14 Hillan, Kenneth J.
 15 Pan, James
 16 Paoni, Nicholas F.
 18 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 19 Acids Encoding the Same
 21 <130> FILE REFERENCE: P2830P1C48
 23 <140> CURRENT APPLICATION NUMBER: 10/015389A
 C--> 24 <141> CURRENT FILING DATE: 2002-06-25
 26 <150> PRIOR APPLICATION NUMBER: 60/098716
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RAW SEQUENCE LISTING

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Input Set : A:\GENENLAW-#104456-v1-

_C48__corrected_sequence_listing.PlC48.txt

Output Set: N:\CRF3\07102002\J015389A.raw

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/015,389A

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Input Set : A:\GENENLAW-#104456-v1-

_C48__corrected_sequence_listing.PlC48.txt

Output Set: N:\CRF3\07102002\J015389A.raw

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RAW SEQUENCE LISTING

DATE: 07/10/2002

PATENT APPLICATION: US/10/015,389A

TIME: 15:15:30

Input Set : A:\GENENLAW-#104456-v1-

_C48__corrected_sequence_listing.PlC48.txt

Output Set: N:\CRF3\07102002\J015389A.raw

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/015,389A

DATE: 07/10/2002

TIME: 15:15:30

Input Set : A:\GENENLAW-#104456-v1-

_C48__corrected_sequence_listing.PlC48.txt

Output Set: N:\CRF3\07102002\J015389A.raw

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/10/2002
PATENT APPLICATION: US/10/015,389A TIME: 15:15:31

Input Set : A:\GENENLAW-#104456-v1-
_C48__corrected_sequence_listing.P1C48.txt
Output Set: N:\CRF3\07102002\J015389A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 233
Seq#:62; N Pos. 678
Seq#:63; Xaa Pos. 196,386
Seq#:259; N Pos. 3635
Seq#:377; N Pos. 396
Seq#:422; N Pos. 1528

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/015,389A

DATE: 07/10/2002

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Input Set : A:\GENENLAW-#104456-v1-
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L:24 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:225
L:3983 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:650
L:4075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:195
L:4111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:375
L:14036 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:259 after pos.:3600
L:20633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:377 after pos.:350
L:22198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:422 after pos.:1500

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/015,389
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ___ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ___ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ___ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ___ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ___ Variable Length	Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ___ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ___ Skipped Sequences (OLD RULES)	Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ___ Skipped Sequences (NEW RULES)	Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ___ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 ___ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <u>375</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ___ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ___ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	